

**What is claimed:**

1. A method for screening a peptide library comprising the steps of,
  - (a) contacting the peptide library with an anti-target to allow the peptides to bind with said anti-target;
  - (b) separating unbound peptides;
  - (c) contacting the unbound peptides with a selected target to allow said unbound peptides to bind with the target to form a target-bound peptide complex;
  - (d) separating said target-bound peptide complex from peptides which do not bind to said target; and
  - (e) identifying the target-bound peptides on the target-bound peptide complex.
2. The method according to claim 1, wherein step (a), (b), (c) or (d) is repeated between 2 to 10 times.
3. A method for screening a peptide library comprising the steps of,
  - (a) contacting the peptide library with a selected target and an anti-target essentially simultaneously to allow the peptides to bind with said target to form a target-bound peptide complex;
  - (b) separating the target-bound peptide complex from the anti-target, anti-target bound peptides and free peptides; and
  - (c) identifying the target-bound peptides on the target-bound peptide complex.
4. The method according to claim 3, wherein said contacting step is *in vivo*.
5. The method according to claim 3, wherein said contacting step is *in vitro*.
6. The method according to claims 1 or 3, wherein the target-bound peptides bind with a selectivity corresponding to at least 10:1 and have a  $K_D$  in the range of at least about  $10^{-7}$  M.
7. The method according to claims 1 or 3, wherein  $k_{off}$  is about  $10^{-4}$  sec<sup>-1</sup> or less.

8. The method according to claims 1 or 3, wherein the identifying step comprises amplifying a nucleic acid coding for the target-bound peptide in a polymerase chain reaction.

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9. The method according to claim 3, wherein the target-bound peptide is not released from the target during the identifying step.

10. The method according to claims 1 or 3, wherein the peptides are fused to a phage coat protein.

11. The method according to claims 1 or 3, wherein separating said target-bound peptide further includes an acid elution step.

12. The method according to claims 1 or 3, wherein the identified target-bound peptides are less than 25 amino acids in length.

13. The method according to claims 1 or 3, wherein the selectivity of the peptide binding affinity to the target compared to the peptide binding affinity to the anti-target is at least 20:1.

14. The method according to claims 1 or 3, wherein the anti-target is skin or hair.

15. The method according to claims 1 or 3, wherein the target is a cytokine selected from the group consisting of TNF and VEGF.

16. The method according to claims 1 or 3, wherein the target is a stain.

17. The method according to claims 1 or 3, wherein the target is a cell surface receptor.

18. The method according to claims 1 or 3, wherein the target is a hematopoietic cell.

19. The method according to claims 1 or 3, wherein the target is a protease enzyme and the anti-target is a different protease enzyme.

20. A peptide identified according to the method of claims 1 or 3.

21. A peptide identified according to the method of claim 15, wherein said peptide has the amino acid sequence of any one sequence of SEQ ID NOS: 3 – 17 or 79 – 102, or  
5 an amino acid sequence having at least 85% sequence identity thereto.

22. A method for identifying peptides useful in a cleaning composition comprising the steps of,

- 10 (a) contacting a peptide library with an anti-target to allow said peptides to bind with the anti-target, wherein the anti-target is selected from the group consisting of fabric, ceramic, glass, stainless steel and plastic;
- (b) separating unbound anti-target peptides;
- 15 (c) contacting said unbound anti-target peptides with a target, wherein the target is a stain selected from the group consisting of porphyrin derived stains, tannin derived stains, carotenoid pigment derived stains, anthocyanin pigment derived stains, soil-based stains, oil-based stains, and human body soil stains to allow said unbound peptides to bind with the stain to form a stain-bound peptide complex; and

20 (d) identifying the stain-bound peptides on the stain-bound peptide complex.

23. The method according to claim 22, wherein the cleaning composition is a detergent composition.

24. A cleaning composition comprising a peptide identified according to claim 22 and  
25 one or more surfactants.

25. The method according to claim 22, wherein the fabric is selected from the group consisting of cotton, wool, silk, polyester, rayon, linen, nylon and blends thereof.

30 26. The method according to claim 22, wherein the stain is selected from the group consisting of blood, chlorophyll, bilirubin, tea, wine, tomato, and berries.

27. A peptide identified according to the method of claim 22, wherein said peptide can bind to the target stain with a  $K_D$  in the range of about  $10^{-7}$  M to  $10^{-10}$  M.

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28. A peptide identified according to the method of claim 22, wherein said peptide has the amino acid sequence of any one sequence of SEQ ID NOs: 18 – 26, or an amino acid sequence having at least 85% sequence identity to any one sequence of SEQ ID NOs: 18 – 26.

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29. A peptide identified according to the method of claim 22, wherein said peptide has the amino acid sequence of any one sequence of SEQ ID NOs: 50 - 63, or an amino acid sequence having at least 85% sequence identity to any one sequence of SEQ ID NOs: 50 - 63.

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30. A peptide identified according to the method of claim 22, wherein said peptide has the amino acid sequence of any one sequence of SEQ ID NOs: 64 – 77, or an amino acid sequence having at least 85% sequence identity to any one sequence of SEQ ID NOs: 64 – 77.

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31. A peptide identified according to the method of claim 22, wherein said peptide has the amino acid sequence of any one sequence of SEQ ID NOs: 29 – 49, or an amino acid sequence having at least 85% sequence identity to any one sequence of SEQ ID NOs: 29 - 49.

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32. A peptide comprising the amino acid sequence of any one sequence of SEQ ID NOs: 103 – 113, or an amino acid sequence having at least 90% sequence identity to any one sequence of SEQ ID NOs: 103 - 113.

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